**Amendments to the Specification**

Please replace the paragraph beginning at page 11, line 13, with the following amended paragraph.

FIGURE 2. Alignment of the N-terminal regions of *E. coli* (SEQ ID NO: 19) and *B. subtilis* (SEQ ID NO: 20) *dnaX* gene product - Asterisks indicate identities. The ATP binding consensus sequence is indicated. The two regions used for PCR primer design are shown in bold.

Please replace the paragraph beginning at page 12, line 11, with the following amended paragraph.

FIGURE 4C depicts the isolated DNA coding sequence for the *dnaX* gene (also present in FIGURES ~~3A and 3B~~ 4A and 4B) in accordance with the invention, and corresponds to SEQ ID NO:3.

Please replace the paragraph beginning at page 12, line 21, with the following amended paragraph.

FIGURE 5. Alignment of the γ/τ ATP binding domains for different bacteria - Dots indicated those residues that are identical to the *E. coli dnaX* sequence. The ATP consensus site is underlined, and the conserved cysteine residues that form the zinc finger are indicated with asterisks. *E. coli, Escherichia coli* (SEQ ID NO: 21); *H. inf., Haemophilus influenzae* (SEQ ID NO: 22); *B. sub., Bacillus subtilis* (SEQ ID NO:23); *C. cres., Caulobacter crescentus* (SEQ ID NO: 24); *M. gen., Mycoplasma genitalium* (SEQ ID NO: 25); *T.th., Thermus theromophilus* (SEQ ID NO: 26). Alignments were produced using ~~Clustel~~ Clustal.

Please replace the paragraph beginning at page 13, line 3, with the following amended paragraph.

FIGURE 6. Signal for ribosomal frameshifting in *T.th. dnaX* - The diagram shows part of the sequence of the RNA (SEQ ID NO: 27) around the frameshifting site (SEQ ID NO: 28), including the suspected slippery sequence A9 (bold italic). The stop codon in the -2 reading frame is indicated. Also indicated are potential step loop structures and the nearest stop codons in the -1 reading frame.

Please replace the paragraph beginning at page 16, line 3, with the following amended paragraph.

FIGURE 16 shows a partial nucleotide (Panel A, SEQ ID NO: 86) and amino acid (Panel B, SEQ ID NO: 87) sequence of the dnaE gene encoding the α subunit of DNA polymerase III holoenzyme. The peptide sequence in bold was obtained by microsequencing of the α subunit isolated from *T.th.* cells.

Please replace the paragraph beginning at page 16, line 7, with the following amended paragraph.

FIGURE 17 shows an alignment of the amino acid sequence of ε subunits encoded by *dnaQ* of several organisms. The amino acid sequence of the *Thermus thermophilus* ε subunit of *dnaQ* is also shown. *T.th., Thermus thermophilus* (SEQ ID NO: 88); *D.rad., Deinococcus radiodurans* (SEQ ID NO: 89); *Bac.sub., Bacillus subtilis* (SEQ ID NO: 90); *H.inf., Haemophilus influenzae* (SEQ ID NO: 91); *E.c., Escherichia coli* (SEQ ID NO: 92); *H.pyl., Helicobacter pylori* (SEQ D NO: 93). The regions used to obtain the inner part of the dnaQ gene are shown in bold. The starts used for expression of the *T.th.* ε subunit are marked.

Please replace the paragraph beginning at page 16, line 14, with the following amended paragraph.

FIGURE 18 shows the nucleotide (Panel A, SEQ ID NO: 94) and amino acid (Panel B, SEQ ID NO: 95) sequence of the dnaQ gene encoding the ε subunit of DNA polymerase III holoenzyme.

Please replace the paragraph beginning at page 16, line 16, with the following amended paragraph.

FIGURE 19 shows an alignment of the DnaA protein of several organisms. The amino acid sequence of the *Thermus thermophilus* DnaA protein of is also shown. *P. mar, Pseudomonas marcesans* (SEQ ID NO: 96); *Syn. sp., Synechocystis sp.* (SEQ ID NO: 97); *Bac. sub., Bacillus subtilies* (SEQ ID NO: 98); *M. tub., Mycobacterium tuberculosis* (SEQ ID NO: 99); *T. th., Thermus thermophilus* (SEQ ID NO: 100); *E. c., Escherichia coli* (SEQ ID NO: 101); *T. mar., Thermotoga maratima* (SEQ ID NO: 102). ~~*T.th., Thermus thermophilus; Bac.sub., Bacillus subtilis; E.c., Escherichia coli; H.pyl., Helicobacter pylori; M. tub; Mycobacterium tuberculosis; T. mar., Thermatoga maritime.*~~

Please replace the paragraph beginning at page 16, line 21, with the following amended paragraph.

FIGURE 20 shows the nucleotide (Panel A, SEQ ID NO: 104) and amino acid (Panel B, SEQ ID NO: 105) sequence of the dnaA gene of *Thermus thermophilus*.

Please replace the paragraph beginning at page 16, line 23, with the following amended paragraph.

FIGURE 21 shows the nucleotide (Panel A, SEQ ID NO: 106) and amino acid (Panel B, SEQ ID NO: 107) sequence of the dnaN gene encoding the ß subunit of DNA polymerase III holoenzyme.

Please replace the paragraph beginning at page 36, line 11 with the following amended paragraph.

Accordingly, the Polymerase III-type enzyme of the present invention comprises at least one gene encoding a ~~sub unit~~ subunit thereof, which gene is selected from the group consisting of ~~dua X, dua Q, dua E and dua N~~ dnaX, dnaQ, dnaE, dnaN, and combinations thereof. More particularly, the invention extends to the nucleic acid molecule encoding them ~~and t~~ and their subunits, and includes the ~~dua X~~ dnaX gene which has a nucleotide sequence as set forth in SEQ ID NO. 3, as well as conserved variants, active fragments and analogs thereof. Likewise, the nucleotide sequences encoding the α ~~sub unit (dna ε gene)~~ subunit (dnaE gene). The ε ~~sub unit~~ subunit (dnaQ gene) and the β ~~sub unit (dna N gene)~~ subunit (dnaN gene) each comprise the ~~nucleo ??????~~ nucleotide sequences as set forth respectively, in SEQ ID ~~NO'S:~~ NOS: 94, 86, and 106, as well as conserved variants, active fragments and analogs thereof.